

y, Pak

KUJH

1652

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/462,845

DATE: 09/24/2001

TIME: 12:08:48

Input Set : A:\GC382-US-seqlist.txt

Output Set: N:\CRF3\09242001\I462845.raw

3 <110> APPLICANT: Estell, David A.
 5 <120> TITLE OF INVENTION: Proteases From Gram-Positive Organisms
 7 <130> FILE REFERENCE: GC382-US
 9 <140> CURRENT APPLICATION NUMBER: US 09/462,845
 10 <141> CURRENT FILING DATE: 2000-01-13
 12 <150> PRIOR APPLICATION NUMBER: PCT/US98/14647
 13 <151> PRIOR FILING DATE: 1998-07-14
 15 <150> PRIOR APPLICATION NUMBER: EP 97305237.7
 16 <151> PRIOR FILING DATE: 1998-07-15
 18 <160> NUMBER OF SEQ ID NOS: 10
 20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1971
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Bacillus subtilis
 27 <400> SEQUENCE: 1

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| 28 | atgaaaaaagc | tgataaaccgc | agacgacatc | acagcgattg | tctctgtgac | cgatcctcaa | 60 |
| 29 | tacgccccag | acggtacccg | tgccgcatat | gtaaaatcac | aagtaaatca | agagaaaagat | 120 |
| 30 | tcgtatacat | caaataatatg | gatctatgaa | acgaaaacgg | gaggatctgt | tccttggaca | 180 |
| 31 | catggagaaa | agcgaagcac | cgacccaaga | tggctccgg | acgggcgcac | gcttgcctt | 240 |
| 32 | atttctgatc | gagaaggcga | tgcggcacag | ctttatatca | tgagcactga | aggcggagaa | 300 |
| 33 | gcaagaaaac | tgactgatat | cccatatggc | gtgtcaaaagc | cgctatggtc | ccggacgggt | 360 |
| 34 | gaatcgattc | tggtcactat | cagtttggga | gagggggaaa | gcattgtatga | ccgagaaaaaa | 420 |
| 35 | acagagcagg | acagctatga | acctgttcaa | gtgcaaggcc | tctcctacaa | acgggacggc | 480 |
| 36 | aaagggctga | cgagaggtgc | gtatgcccag | cttgcgttgc | tcagcgtaaa | gtcgggttag | 540 |
| 37 | atgaaaagagc | tgacaagtca | caaagctgat | catggtgatc | ctgcgttttc | tcctgacggc | 600 |
| 38 | aaatggctt | tttttcagc | taattttaact | gaaacagatg | atgcagcaa | gccgcatgt | 660 |
| 39 | gtttacataa | tgtcacttgg | gtctggagat | cttaagcagg | ttacacctca | tcggggctca | 720 |
| 40 | ttcggatcaa | gctcatttc | accagacgaa | agttatcttgc | cttgcgttgg | aatgaaaaag | 780 |
| 41 | gaatataaga | atgctacgct | ctcaaaggcg | tggctctatg | atatcgaaaca | aggcgcgc | 840 |
| 42 | acatgtctta | ctgagatgct | ggacgttcat | ttagcggatg | cgctgattgg | agattcattt | 900 |
| 43 | atcggtggtg | ctgaacagcg | cccgattttgg | acaaaggaca | gccaagggtt | ttatgtcatc | 960 |
| 44 | ggcacagatc | aaggcagttac | gggcatttat | tatatttgc | ttgaaggcct | tgtgtatccg | 1020 |
| 45 | attcgtctgg | aaaaagagta | catcaatagc | ttttctcttt | cacctgatga | acagcacttt | 1080 |
| 46 | attgccagtg | tgacaaagcc | ggacagacgg | agttagctt | acagtatccc | gttggacag | 1140 |
| 47 | gaagagaaaac | agctgactgg | cgcgaatgac | aagtttgc | gggagcatac | gatataata | 1200 |
| 48 | cctgaagaga | ttcaatatgc | tacagaagac | ggcgtgatgg | tgaacggctg | gctgtatgagg | 1260 |
| 49 | cctgcacaaa | ttgaaggtga | gacaacatat | ccacttattc | ttaacataca | cgccggcc | 1320 |
| 50 | catatgtatgt | acggacatac | atatttcat | gagtttcagg | tgctggccgc | gaaaggatac | 1380 |
| 51 | gcggtcgttt | atataatcc | gagaggaagc | cacggctacg | ggcaggaatt | tgtaatgcg | 1440 |
| 52 | gtcagaggag | attatggggg | aaaggattat | gacgatgtga | tgcaggctgt | ggatgaggct | 1500 |
| 53 | atcaaacgag | atccgcata | tgatcctaag | cggtcggtg | tcacggccgg | aagctacgga | 1560 |
| 54 | gtttttatga | ccaaactggat | cgtcggcag | acgaaccgct | ttaaagctgc | cggttacccag | 1620 |
| 55 | cgctcgatata | caaattggat | cagcttccac | ggcgtcagtg | atatcggtca | tttctttaca | 1680 |
| 56 | gactggcagc | ttgagcatga | catgtttgag | gacacagaaa | agctctggga | ccggctcc | 1740 |
| 57 | ttaaaatacg | cagcaaacgt | ggagacaccc | cttttgatac | tgcgttgcga | gcggatgac | 1800 |
| 58 | cgatgcccga | tcgagcaggc | ggagcagctg | tttacgctc | tgaaaaaaat | ggcaaggaa | 1860 |

ENTERED

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59 accaagcttg tccgtttcc gaatgcacg cacaatttat cacgcacccgg acacccaaga 1920
 60 cagcgatca agccctgaa ttatatcagc tcatggtttgc atcaacatct c 1971
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 63 <211> LENGTH: 657
 64 <212> TYPE: PRT
 65 <213> ORGANISM: *Bacillus subtilis*
 67 <400> SEQUENCE: 2
 68 Met Lys Leu Ile Thr Ala Asp Asp Ile Thr Ala Ile Val Ser Val
 69 1 5 10 15
 70 Thr Asp Pro Gln Tyr Ala Pro Asp Gly Thr Arg Ala Ala Tyr Val Lys
 71 20 25 30
 72 Ser Gln Val Asn Gln Glu Lys Asp Ser Tyr Thr Ser Asn Ile Trp Ile
 73 35 40 45
 74 Tyr Glu Thr Lys Thr Gly Gly Ser Val Pro Trp Thr His Gly Glu Lys
 75 50 55 60
 76 Arg Ser Thr Asp Pro Arg Trp Ser Pro Asp Gly Arg Thr Leu Ala Phe
 77 65 70 75 80
 78 Ile Ser Asp Arg Glu Gly Asp Ala Ala Gln Leu Tyr Ile Met Ser Thr
 79 85 90 95
 80 Glu Gly Gly Ala Arg Lys Leu Thr Asp Ile Pro Tyr Gly Val Ser
 81 100 105 110
 82 Lys Pro Leu Trp Ser Pro Asp Gly Glu Ser Ile Leu Val Thr Ile Ser
 83 115 120 125
 84 Leu Gly Glu Gly Glu Ser Ile Asp Asp Arg Glu Lys Thr Glu Gln Asp
 85 130 135 140
 86 Ser Tyr Glu Pro Val Glu Val Gln Gly Leu Ser Tyr Lys Arg Asp Gly
 87 145 150 155 160
 88 Lys Gly Leu Thr Arg Gly Ala Tyr Ala Gln Leu Val Leu Val Ser Val
 89 165 170 175
 90 Lys Ser Gly Glu Met Lys Glu Leu Thr Ser His Lys Ala Asp His Gly
 91 180 185 190
 92 Asp Pro Ala Phe Ser Pro Asp Gly Lys Trp Leu Val Phe Ser Ala Asn
 93 195 200 205
 94 Leu Thr Glu Thr Asp Asp Ala Ser Lys Pro His Asp Val Tyr Ile Met
 95 210 215 220
 96 Ser Leu Glu Ser Gly Asp Leu Lys Gln Val Thr Pro His Arg Gly Ser
 97 225 230 235 240
 98 Phe Gly Ser Ser Phe Ser Pro Asp Gly Arg Tyr Leu Ala Leu Leu
 99 245 250 255
 100 Gly Asn Glu Lys Glu Tyr Lys Asn Ala Thr Leu Ser Lys Ala Trp Leu
 101 260 265 270
 102 Tyr Asp Ile Glu Gln Gly Arg Leu Thr Cys Leu Thr Glu Met Leu Asp
 103 275 280 285
 104 Val His Leu Ala Asp Ala Leu Ile Gly Asp Ser Leu Ile Gly Gly Ala
 105 290 295 300
 106 Glu Gln Arg Pro Ile Trp Thr Lys Asp Ser Gln Gly Phe Tyr Val Ile
 107 305 310 315 320
 108 Gly Thr Asp Gln Gly Ser Thr Gly Ile Tyr Tyr Ile Ser Ile Glu Gly
 109 325 330 335

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110 Leu Val Tyr Pro Ile Arg Leu Glu Lys Glu Tyr Ile Asn Ser Phe Ser
 111 340 345 350
 112 Leu Ser Pro Asp Glu Gln His Phe Ile Ala Ser Val Thr Lys Pro Asp
 113 355 360 365
 114 Arg Pro Ser Glu Leu Tyr Ser Ile Pro Leu Gly Gln Glu Glu Lys Gln
 115 370 375 380
 116 Leu Thr Gly Ala Asn Asp Lys Phe Val Arg Glu His Thr Ile Ser Ile
 117 385 390 395 400
 118 Pro Glu Glu Ile Gln Tyr Ala Thr Glu Asp Gly Val Met Val Asn Gly
 119 405 410 415
 120 Trp Leu Met Arg Pro Ala Gln Met Glu Gly Glu Thr Thr Tyr Pro Leu
 121 420 425 430
 122 Ile Leu Asn Ile His Gly Gly Pro His Met Met Tyr Gly His Thr Tyr
 123 435 440 445
 124 Phe His Glu Phe Gln Val Leu Ala Ala Lys Gly Tyr Ala Val Val Tyr
 125 450 455 460
 126 Ile Asn Pro Arg Gly Ser His Gly Tyr Gly Gln Glu Phe Val Asn Ala
 127 465 470 475 480
 128 Val Arg Gly Asp Tyr Gly Gly Lys Asp Tyr Asp Asp Val Met Gln Ala
 129 485 490 495
 130 Val Asp Glu Ala Ile Lys Arg Asp Pro His Ile Asp Pro Lys Arg Leu
 131 500 505 510
 132 Gly Val Thr Gly Gly Ser Tyr Gly Gly Phe Met Thr Asn Trp Ile Val
 133 515 520 525
 134 Gly Gln Thr Asn Arg Phe Lys Ala Ala Val Thr Gln Arg Ser Ile Ser
 135 530 535 540
 136 Asn Trp Ile Ser Phe His Gly Val Ser Asp Ile Gly Tyr Phe Phe Thr
 137 545 550 555 560
 138 Asp Trp Gln Leu Glu His Asp Met Phe Glu Asp Thr Glu Lys Leu Trp
 139 565 570 575
 140 Asp Arg Ser Pro Leu Lys Tyr Ala Ala Asn Val Glu Thr Pro Leu Leu
 141 580 585 590
 142 Ile Leu His Gly Glu Arg Asp Asp Arg Cys Pro Ile Glu Gln Ala Glu
 143 595 600 605
 144 Gln Leu Phe Ile Ala Leu Lys Lys Met Gly Lys Glu Thr Lys Leu Val
 145 610 615 620
 146 Arg Phe Pro Asn Ala Ser His Asn Leu Ser Arg Thr Gly His Pro Arg
 147 625 630 635 640
 148 Gln Arg Ile Lys Arg Leu Asn Tyr Ile Ser Ser Trp Phe Asp Gln His
 149 645 650 655
 150 Leu
 152 <210> SEQ ID NO: 3
 153 <211> LENGTH: 818
 154 <212> TYPE: PRT
 155 <213> ORGANISM: Bacillus subtilis
 157 <400> SEQUENCE: 3
 158 Met Glu Gly Gly Glu Glu Val Glu Arg Ile Pro Asp Glu Leu Phe
 159 1 5 10 15
 160 Asp Thr Lys Lys His Leu Leu Asp Lys Leu Ile Arg Val Gly Ile

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| | | | |
|-----|---|-----|-----|
| 161 | 20 | 25 | 30 |
| 162 | Ile Leu Val Leu Leu Ile Trp Gly Thr Val Leu Leu Leu Lys Ser Ile | | |
| 163 | 35 | 40 | 45 |
| 164 | Pro His His Ser Asn Thr Pro Asp Tyr Gln Glu Pro Asn Ser Asn Tyr | | |
| 165 | 50 | 55 | 60 |
| 166 | Thr Asn Asp Gly Lys Leu Lys Val Ser Phe Ser Val Val Arg Asn Asn | | |
| 167 | 65 | 70 | 75 |
| 168 | 80 | | |
| 169 | Thr Phe Gln Pro Lys Tyr His Glu Leu Gln Trp Ile Ser Asp Asn Lys | | |
| 170 | 85 | 90 | 95 |
| 171 | Ile Glu Ser Asn Asp Leu Gly Leu Tyr Val Thr Phe Met Asn Asp Ser | | |
| 172 | 100 | 105 | 110 |
| 173 | Tyr Val Val Lys Ser Val Tyr Asp Asp Ser Tyr Asn Ser Val Leu Leu | | |
| 174 | 115 | 120 | 125 |
| 175 | Glu Gly Lys Thr Phe Ile His Asn Gly Gln Asn Leu Thr Val Glu Ser | | |
| 176 | 130 | 135 | 140 |
| 177 | Ile Thr Ala Ser Pro Asp Leu Lys Arg Leu Leu Ile Arg Thr Asn Ser | | |
| 178 | 145 | 150 | 155 |
| 179 | 160 | | |
| 180 | Val Gln Asn Trp Arg His Ser Thr Phe Gly Ser Tyr Phe Val Tyr Asp | | |
| 181 | 165 | 170 | 175 |
| 182 | Lys Ser Ser Ser Phe Glu Glu Ile Gly Asn Glu Val Ala Leu Ala | | |
| 183 | 180 | 185 | 190 |
| 184 | Ile Trp Ser Pro Asn Ser Asn Asp Ile Ala Tyr Val Gln Asp Asn Asn | | |
| 185 | 195 | 200 | 205 |
| 186 | Ile Tyr Ile Tyr Ser Ala Ile Ser Lys Lys Thr Ile Arg Ala Val Thr | | |
| 187 | 210 | 215 | 220 |
| 188 | Asn Asp Gly Ser Ser Phe Leu Phe Asn Gly Lys Pro Asp Trp Val Tyr | | |
| 189 | 225 | 230 | 235 |
| 190 | 240 | | |
| 191 | Glu Glu Glu Val Phe Glu Asp Asp Lys Ala Ala Trp Trp Ser Pro Thr | | |
| 192 | 245 | 250 | 255 |
| 193 | Gly Asp Tyr Leu Ala Phe Leu Lys Ile Asp Glu Ser Glu Val Gly Glu | | |
| 194 | 260 | 265 | 270 |
| 195 | Phe Ile Ile Pro Tyr Tyr Val Gln Asp Glu Lys Asp Ile Tyr Pro Glu | | |
| 196 | 275 | 280 | 285 |
| 197 | 290 | 295 | 300 |
| 198 | Met Arg Ser Ile Lys Tyr Pro Lys Ser Gly Thr Pro Asn Pro His Ala | | |
| 199 | 305 | 310 | 315 |
| 200 | 320 | | |
| 201 | Glu Leu Trp Val Tyr Ser Met Lys Asp Gly Thr Ser Phe His Pro Arg | | |
| 202 | 325 | 330 | 335 |
| 203 | Ile Ser Gly Asn Lys Lys Asp Gly Ser Leu Leu Ile Thr Glu Val Thr | | |
| 204 | 340 | 345 | 350 |
| 205 | Trp Val Gly Asn Gly Asn Val Leu Val Lys Thr Thr Asp Arg Ser Ser | | |
| 206 | 355 | 360 | 365 |
| 207 | Val Val Arg Asn Glu Ser Ser Asn Gly Gly Trp Trp Glu Ile Thr His | | |
| 208 | 370 | 375 | 380 |
| 209 | Asn Thr Leu Phe Ile Pro Ala Asn Glu Thr Phe Asp Arg Pro His Asn | | |
| | 385 | 390 | 395 |
| | 400 | | |
| | Gly Tyr Val Asp Ile Leu Pro Ile Gly Gly Tyr Asn His Leu Ala Tyr | | |
| | 405 | 410 | 415 |

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210 Phe Glu Asn Ser Asn Ser Ser His Tyr Lys Thr Leu Thr Glu Gly Lys
 211 420 425 430
 212 Trp Glu Val Val Asn Gly Pro Leu Ala Phe Asp Ser Met Glu Asn Arg
 213 435 440 445
 214 Leu Tyr Phe Ile Ser Thr Arg Lys Ser Ser Thr Glu Arg His Val Tyr
 215 450 455 460
 216 Tyr Ile Asp Leu Arg Ser Pro Asn Glu Ile Ile Glu Val Thr Asp Thr
 217 465 470 475 480
 218 Ser Glu Asp Gly Val Tyr Asp Val Ser Phe Ser Ser Gly Arg Arg Phe
 219 485 490 495
 220 Gly Leu Leu Thr Tyr Lys Gly Pro Lys Val Pro Tyr Gln Lys Ile Val
 221 500 505 510
 222 Asp Phe His Ser Arg Lys Ala Glu Lys Cys Asp Lys Gly Asn Val Leu
 223 515 520 525
 224 Gly Lys Ser Leu Tyr His Leu Glu Lys Asn Glu Val Leu Thr Lys Ile
 225 530 535 540
 226 Leu Glu Asp Tyr Ala Val Pro Arg Lys Ser Phe Arg Glu Leu Asn Leu
 227 545 550 555 560
 228 Gly Lys Asp Glu Phe Gly Lys Asp Ile Leu Val Asn Ser Tyr Glu Ile
 229 565 570 575
 230 Leu Pro Asn Asp Phe Asp Glu Thr Leu Ser Asp His Tyr Pro Val Phe
 231 580 585 590
 232 Phe Phe Ala Tyr Gly Gly Pro Asn Ser Gln Gln Val Val Lys Thr Phe
 233 595 600 605
 234 Ser Val Gly Phe Asn Glu Val Val Ala Ser Gln Leu Asn Ala Ile Val
 235 610 615 620
 236 Val Val Val Asp Gly Arg Gly Thr Gly Phe Lys Gly Gln Asp Phe Arg
 237 625 630 635 640
 238 Ser Leu Val Arg Asp Arg Leu Gly Asp Tyr Glu Ala Arg Asp Gln Ile
 239 645 650 655
 240 Ser Ala Ala Ser Leu Tyr Gly Ser Leu Thr Phe Val Asp Pro Gln Lys
 241 660 665 670
 242 Ile Ser Leu Phe Gly Trp Ser Tyr Gly Gly Tyr Leu Thr Leu Lys Thr
 243 675 680 685
 244 Leu Glu Lys Asp Gly Gly Arg His Phe Lys Tyr Gly Met Ser Val Ala
 245 690 695 700
 246 Pro Val Thr Asp Trp Arg Phe Tyr Asp Ser Val Tyr Thr Glu Arg Tyr
 247 705 710 715 720
 248 Met His Thr Pro Gln Glu Asn Phe Asp Gly Tyr Val Glu Ser Ser Val
 249 725 730 735
 250 His Asn Val Thr Ala Leu Ala Gln Ala Asn Arg Phe Leu Leu Met His
 251 740 745 750
 252 Gly Thr Gly Asp Asp Asn Val His Phe Gln Asn Ser Leu Lys Phe Leu
 253 755 760 765
 254 Asp Leu Leu Asp Leu Asn Gly Val Glu Asn Tyr Asp Val His Val Phe
 255 770 775 780
 256 Pro Asp Ser Asp His Ser Ile Arg Tyr His Asn Ala Asn Val Ile Val
 257 785 790 795 800
 258 Phe Asp Lys Leu Leu Asp Trp Ala Lys Arg Ala Phe Asp Gly Gln Phe

VERIFICATION SUMMARY

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